Resource Summary Report

Generated by NIF on Apr 26, 2025

leeHom

RRID:SCR_002710
Type: Tool

Proper Citation

leeHom (RRID:SCR_002710)

Resource Information

URL: https://github.com/grenaud/leeHom

Proper Citation: leeHom (RRID:SCR_002710)

Description: Software program for the Bayesian reconstruction of ancient DNA fragments. The algorithm removes the adaptors and reconstructs the original DNA sequences using a Bayesian maximum a posteriori probability approach.

Resource Type: software resource

Defining Citation: PMID:25100869

Keywords: standalone software, illumina, bio.tools

Funding:

Resource Name: leeHom

Resource ID: SCR_002710

Alternate IDs: biotools:leehom, OMICS_05254

Alternate URLs: https://bio.tools/leehom

Record Creation Time: 20220129T080214+0000

Record Last Update: 20250420T014118+0000

Ratings and Alerts

No rating or validation information has been found for leeHom.

No alerts have been found for leeHom.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 44 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Zhang M, et al. (2024) Ancient Mitogenomes Reveal the Maternal Genetic History of East Asian Dogs. Molecular biology and evolution, 41(4).

Michel M, et al. (2024) Ancient Plasmodium genomes shed light on the history of human malaria. Nature, 631(8019), 125.

Bai F, et al. (2024) Ancient genomes revealed the complex human interactions of the ancient western Tibetans. Current biology : CB, 34(12), 2594.

Diaz Quiroz JF, et al. (2023) Development of a selection assay for small guide RNAs that drive efficient site-directed RNA editing. Nucleic acids research, 51(7), e41.

Woravatin W, et al. (2023) South Asian maternal and paternal lineages in southern Thailand and the role of sex-biased admixture. PloS one, 18(9), e0291547.

Wang H, et al. (2023) Human genetic history on the Tibetan Plateau in the past 5100 years. Science advances, 9(11), eadd5582.

Essel E, et al. (2023) Ancient human DNA recovered from a Palaeolithic pendant. Nature, 618(7964), 328.

Lien A, et al. (2023) Benchmarking software tools for trimming adapters and merging next-generation sequencing data for ancient DNA. Frontiers in bioinformatics, 3, 1260486.

Yilmaz F, et al. (2023) Ancient AMY1 gene duplications primed the amylase locus for adaptive evolution upon the onset of agriculture. bioRxiv : the preprint server for biology.

Cohen P, et al. (2023) Ancient DNA from a lost Negev Highlands desert grape reveals a Late Antiquity wine lineage. Proceedings of the National Academy of Sciences of the United States of America, 120(17), e2213563120.

Hodgins HP, et al. (2023) Ancient Clostridium DNA and variants of tetanus neurotoxins associated with human archaeological remains. Nature communications, 14(1), 5475.

Irie N, et al. (2023) DMRT1 regulates human germline commitment. Nature cell biology, 25(10), 1439.

Li YC, et al. (2023) Mitogenome evidence shows two radiation events and dispersals of matrilineal ancestry from northern coastal China to the Americas and Japan. Cell reports, 42(5), 112413.

Massilani D, et al. (2022) Microstratigraphic preservation of ancient faunal and hominin DNA in Pleistocene cave sediments. Proceedings of the National Academy of Sciences of the United States of America, 119(1).

Bennett EA, et al. (2022) The genetic identity of the earliest human-made hybrid animals, the kungas of Syro-Mesopotamia. Science advances, 8(2), eabm0218.

Renaud G, et al. (2022) Unsupervised detection of fragment length signatures of circulating tumor DNA using non-negative matrix factorization. eLife, 11.

Brown S, et al. (2022) The earliest Denisovans and their cultural adaptation. Nature ecology & evolution, 6(1), 28.

Zhang X, et al. (2022) A Late Pleistocene human genome from Southwest China. Current biology : CB, 32(14), 3095.

Mao X, et al. (2021) The deep population history of northern East Asia from the Late Pleistocene to the Holocene. Cell, 184(12), 3256.

Rusman F, et al. (2021) Guide RNA Repertoires in the Main Lineages of Trypanosoma cruzi: High Diversity and Variable Redundancy Among Strains. Frontiers in cellular and infection microbiology, 11, 663416.